β1α1

ع د	Ncol CATE	<u>.</u> <u>.</u> <u>.</u>	CAGA	ĢAC	TCC	V CCA	\AG0	GAT	TTC	GTO	TAC	CAC	STTC	AAC	GGG	CTC	TGC	TAC	TAC	ACC	
-2	М	G	R	D	s	P	R	D	F	V	Y	Q	F	.+	G	L	C	Y	Y	+	60
61	AACGGGACGCAGCGCATACGGGATGTGATCAGATACATCTACAACCAGGAGGAGTACCTG																				
	N	G	т	Q	R	I	R	D			R					Q		E	Y	+	120
121	CGC	CGCTACGACAGCGACGTGGGCGAGTACCGCGCGCTGACCGAGCTGGGGCGGCCCTCAGCC																			
	R	Y	D	S	D	v	Ğ	E	Y		A			+	L	G	-+- R	P		+ A	180
181	GAG	GAGTACTTTAACAAGCAGTACCTGGAGCAGACGCGGGCCGAGCTGGACACGGTCTGCAGA																			
	E	Y	F	N	ĸ	Q	Ϋ́	L	E	Q	- <u>-</u> -	R		+	L		-+- T	~~=	C	 +	240
241	end of \$1 ▼ start of α1 CACAACTACGAGGGTCGGAGGTCCGCACCTCCCTGCGGCGGCTTGGAGGTCAAGACGAC H N Y E G S E V R T S L R R L G G Q D D															200					
	Н	N	Y	E	G	s	É	v	R	T	s		R	R	L	G	-+- G	Q	D	+ D	300
301	ATT	ATTGAGGCCGACCACGTAGCCGCCTATGGTATAAATATGTATCAGTATTATGAATCCAGA																			
	I	Ε	A	D	Н	v	-+- A	A	Y	G	I	N	M	+	Q	Y	-+- Y	E	s	R	360
361	GGC	GGCCAGTTCACACATGAATTTGATGGTGACGAGGAATTCTATGTGGACTTGGATAAGAAG																			
	G	Q	F	T	Н	E	F .	D	G	D+	E	Ε	F	+		D	_+-	D	- <u>-</u>	+ K	420
421	GAGACCATCTGGAGGATCCCCGAGTTTGGACAGCTGACAAGCTTTGACCCCCAAGGTGGA																				
	Ε			⊬	R	I	-+ P	E	F	G +	Q	L	T	+ S	F	D	-+-: P	0		+ G	480
481	المنشار	CTTCAAAATATAGCTATAATAAAACACAATTTGGAAATCTTGATGAAGAGGTCAAATTCA																			
	L	0	N	I	A	I	-+	K	-AC/	 Н	L	3AA. E			arg/ M	AAGA K	4GG'	rca.			540
	_	_	••	-			Xho	ΣĪ	**	11	ш	نا	. т	ы	PL	V	ĸ	S	И	S	
541	ACCO						TC:	AG													
	1	Q	A	V	N e	end															

FIG. 1A

1/15

 β 1 α 1/MBP-72-89

FIG. 1B

<u>ccatgg</u>gcagagactccccacagagagccagaggactcaggatgagacccagtggtggtgcacttcggaggtggaggctc<u>actagt</u>gccccgaggctct |--1inker---|----thrombin----Q D E N P V V H F G G G G S L V P R \$101/MBP-55-69 GGAGGTGGAGGCTCC G G G G S |--1inker---|

FIG. 1D

FIG. 1C

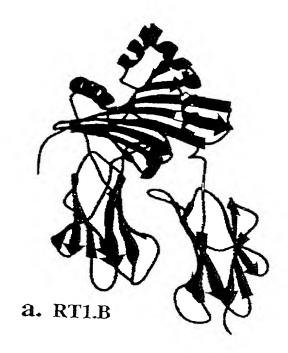
<u>ccatgg</u>gcagagactccaaactggaactgcagtccgctctggaagatgaagcttgaagcttcctggaacacggaggtggaggctc<u>actagt</u>g

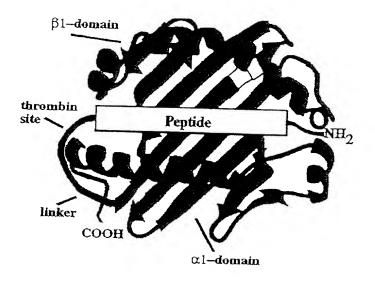
MGRDSKLELQSALE

ပ

o3

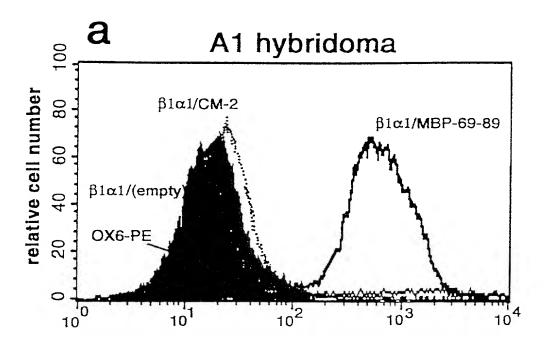
덟 < 띠





b. $\beta 1\alpha 1/\text{peptide}$

FIG. 2 3/15



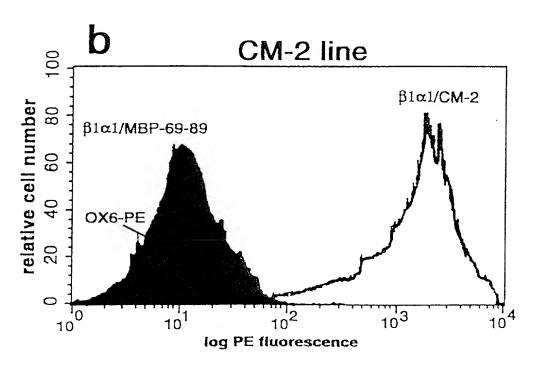


FIG. 3 4/15

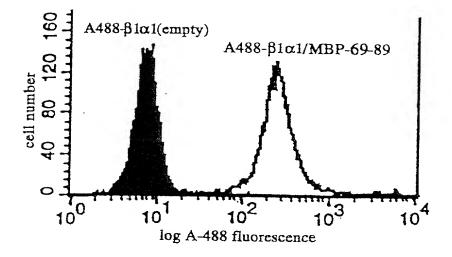


FIG. 4 5/15

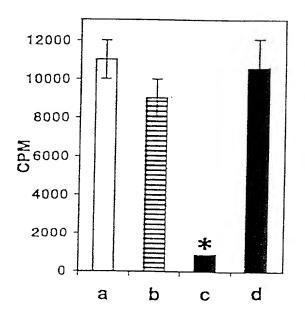
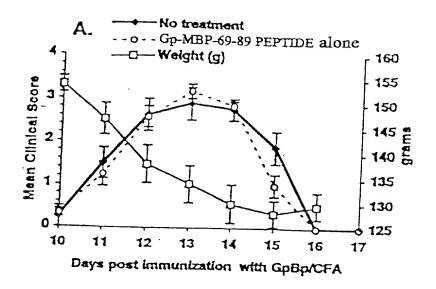


FIG. 5 6/15



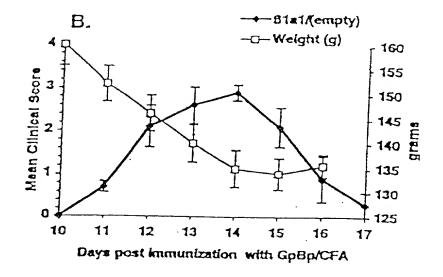
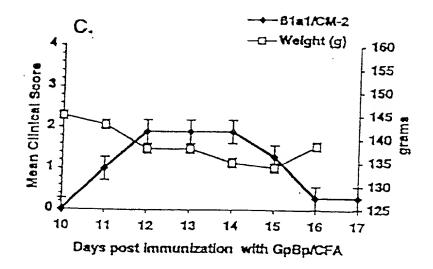


FIG. 6A 7/15



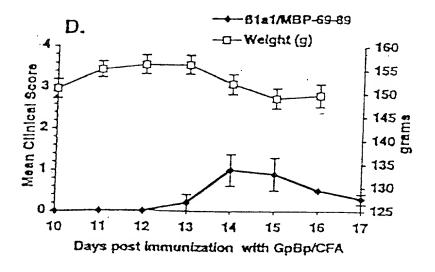


FIG. 6B 8/15

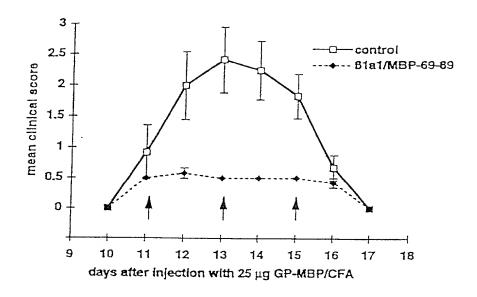
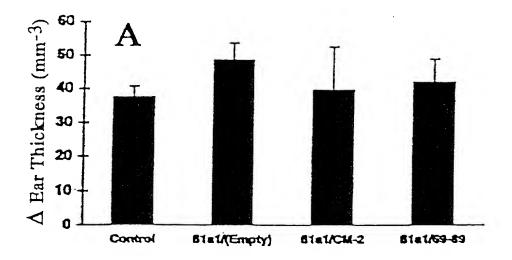


FIG. 7 9/15



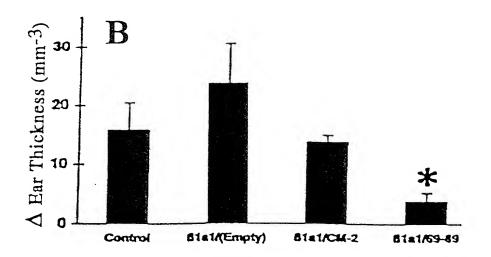


FIG. 8 10/15

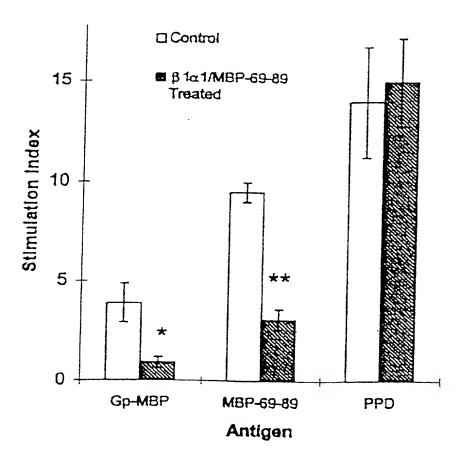


FIG. 9 11/15

βl domain:

ARG4-PRO5-ARG6-PHE7-LEU8-TRP9-GLN10-LEU11-LYS12-PHE13-GLU14-CYS15-HIS16-PHE17-PHE18-ASN19-GLY20-THR21-GLU22-ARG23-VAL24-ARG25-LEU26-LEU27-GLU28-ARG29-CYS30-ILE31-TYR32-ASN33-GLN34-GLU35-GLU36-SER37-VAL38-ARG39-PHE40-ASP41-SER42-ASP43-VAL44-GLY45-GLU46-TYR47-ARG48-ALA49-VAL50-THR51-GLU52-LEU53-GLY54-ARG55-PRO56-ASP57-ALA58-GLU59-TYR60-TRP61-ASN62-SER63-GLN64-LYS65-ASP66-LEU67-LEU68-GLU69-GLN70-ARG71-ARG72-ALA73-ALA74-VAL75-ASP76-THR77-TYR78-CYS79-ARG80-HIS81-ASN82-TYR83-GLY84-VAL85-GLY86-GLU87-SER88-PHE89-THR90-VAL91-GLN92-ARG93-ARG94-VAL95

ASN15-PRO16-ASP17-GLN18-SER19-GLY20-GLU21-PHE22-MET23-PHE24-ASP25-PHE26-ASP27-GLY28-ASP29-GLU30-ILE31-PHE32-HIS33-VAL34-ASP35-MET36-ALA37-LYS38-LYS39-GLU40-THR41-VAL42-TRP43-ARG44-LEU45-GLU46-GLU47-PHE48-GLY49-ARG50-PHE51-ALA52-SER53-PHE54-GLU55-ALA56-GLN57-GLY58-ALA59-LEU60-ALA61-ASN62-ILE63-ALA64-VAL65-ASP66-LYS67-ALA68-ASN69-LEU70-GLU71-ILE72-MET73-THR74-LYS75-ARG76-SER77-ASN78-TYR79-THR80-GLU3-GLU4-HIS5-VAL6-ILE7-ILE8-GLN9-ALA10-GLU11-PHE12-TYR13-LEU14-PRO81-ILE82-THR83-ASN84 αl domain:

FIG. 10A 12/15

βl domain;

ARG4~PRO5-TRP6~PHE7-LEU8-GLU9-TYR10-CYS11-LYS12-SER13-GLU14-CYS15-HIS16-PHE17-TYR18-ASN19-GLY20-THR21-GLN22-ARG23-VAL24-ARG25-LEU26-LEU27-VAL28-ARG29-TYR30-PHE31-TYR32-ASN33-LEU34-GLU35-GLU36-ASN37-LEU38-ARG39-PHE40-ASP41-SER42-ASP43-VAL44-GLY45-GLU46-PHE47-ARG48-ALA49-VAL50-THR51-GLU52-LEU53-GLY54-ARG55-PR056-ASP57-ALA58-GLU59-ASN60-TRP61-ASN62-SER63-GLN64-PRO65-GLU66-PHE67-LEU68-GLU69-GLN70-LYS71-ARG72-ALA73-GLU74-VAL75-ASP76-THR77-VAL78-CYS79-ARG80-HIS81-ASN82-TYR83-GLU84-ILE85-PHE86-ASP87-ASN88-PHE89-LEU90-VAL91-PRO92-

α1 domain;

LEU15-PRO16-ASP17-LYS18-ARG19-GLY20-GLU21-PHE22-MET23-PHE24-ASP25-PHE26-ASP27-GLY28-ASP29-GLU30-ILE31-PHE32-HIS33-VAL34-ASP35-ILE36-GLU37-LYS38-SER39-GLU40-THR41-ILE42-TRP43-ARG44-LEU45-GLU46-GLU47-PHE48-ALA49-LYS50-PHE51-ALA52-SER53-PHE54-GLU55-ALA56-GLN57-GLY58-ALA59-LEU60-ALA61-ASN62-ILE63-ALA64-VAL65-ASP66-LYS67-ALA68-ASN69-LEU70-ASP71-VAL72-MET73-LYS74-GLU75-ARG76-SER77-ASN78-ASN79-THR80-GLU3-GLU4-HIS5-THR6-ILE7-ILE8-GLN9-ALA10-GLU11-PHE12-TYR13-LEU14-

FIG. 10B 13/15

βl domain;

THR21-GLN22-ARG23-ILE24-ARG25-ASP26-VAL27-ILE28-ARG29-TYR30-ILE31-GLN10-PHE11-LYS12-GLY13-LEU14-CYS15-TYR16-TYR17-THR18-ASN19-GLY20-TYR32-ASN33-GLN34-GLU35-GLU36-TYR37-LEU38-ARG39-TYR40-ASP41-SER42-ASP43-VAL44-GLY45-GLU46-TYR47-ARG48-ALA49-LEU50-THR51-GLU52-LEU53-GLY54-ARG55-PRO56-SER57-ALA58-GLU59-TYR60-TRP61-ASN62-SER63-GLN64-LYS65-GLN66-TYR67-LEU68-GLU69-GLN70-THR71-ARG72-ALA73-GLU74-LEU75-ASP76-THR77-VAL78-CYS79-ARG80-HIS81-ASN82-TYR83-GLU84-GLY85-SER86-MET (-2)-GLY (-1)-ARG1-ASP2-SER3-PRO4-ARG5-ASP6-PHE7-VAL8-TYR9-GLU87~VAL88-ARG89-THR90-SER91-LEU92-ARG93-ARG94-LEU95

 $\alpha 1$ domain:

GLN14-TYR15-TYR16-GLU17-SER18-ARG19-GLY20-GLN21-PHE22-THR23-HIS24-GLU25-PHE26-ASP27-GLY28-ASP29-GLU30-GLU31-PHE32-TYR33-VAL34-ASP35-LEU36-ASP37-LYS38-LYS39-GLU40-THR41-ILE42-TRP43-ARG44-ILE45-PRO46-GLU47-PHE48-GLY49-GLN50-LEU51-THR52-SER53-PHE54-ASP55-PRO56-GLN57-GLY58-GLY59-LEU60-GLN61-ASN62-ILE63-ALA64-ILE65-ILE66-LYS67-HIS68-ASN69-LEU70-GLU71-ILE72-LEU73-MET74-LYS75-ARG76-SER77-ASN78-SER79-ALA2-ASP3-HIS4-VAL5-ALA6-ALA7-TYR8-GLY9-ILE10-ASN11-MET12-TYR13-THR80-GLN81-ALA82-VAL83-ASN84

FIG. 10C 14/15

αl domain:

SER13-ARG14-PRO15-GLY16-ARG17-GLY18-GLU19-PRO20-ARG21-PHE22-ILE23-GLU46-PRO47-ARG48-PRO49-PRO50-TRP51-ILE52-GLU53-GLN54-GLU55-GLY56-PRO57-GLU58-TYR59-TRP60-ASP61-ARG62-ASN63-THR64-GLN65-ILE66-PHE67-ARG35-PHE36-ASP37-SER38-ASP39-ALA40-ALA41-SER42-PRO43-ARG44-THR45-ALA24-VAL25-GLY26-TYR27-VAL28-ASP29-ASP30-THR31-GLN32-PHE33-VAL34 LYS68-THR69-ASN70-THR71-GLN72-THR73-TYR74-ARG75-GLU76-ASN77-LEU78-GLY1-SER2-HIS3-SER4-MET5-ARG6-TYR7-PHE8-TYR9-THR10-ALA11-MET12-ARG79-ILE80-ALA81-LEU82-ARG83-TYR84-

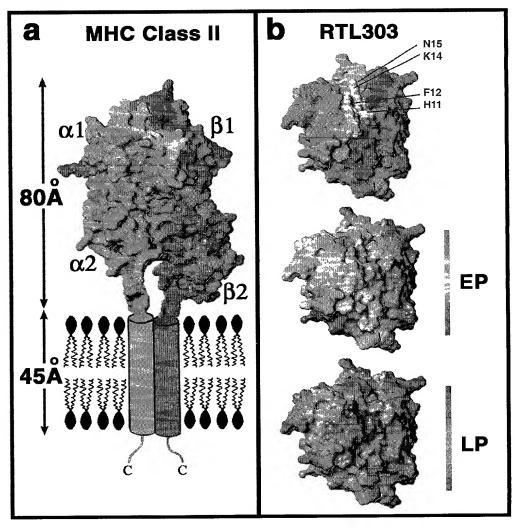
α2 domain:

TYR85-ASN86-GLN87-SER88-GLU89-ALA90-GLY91-SER92-HIS93-ILE94-ILE95-GLN96-ARG97-MET98-TYR99-GLY100-CYS101-ASP102-LEU103-GLY104-PRO105-ILE124-ALA125-LEU126-ASN127-GLU128-ASP129-LEU130-SER131-SER132-TRP133-THR134-ALA135-ALA136-ASP137-THR138-ALA139-ALA140-GLN141-ASP106-GLY107-ARG108-LEU109-LEU110-ARG111-GLY112-HIS113-ASP114-ILE142-THR143-GLN144-ARG145-LYS146-TRP147-GLU148-ALA149-ALA150-ARG151-VAL152-ALA153-GLU154-GLN155-LEU156-ARG157-ALA158-TYR159-LEU1 60-GLU1 61-GLY1 62-LEU1 63-CYS1 64-VAL1 65-GLU1 66-TRP1 67-LEU1 68-ARG169-ARG170-TYR171-LEU172-GLU173-ASN174-GLY175-LYS176-GLU177-GLN115-SER116-ALA117-TYR118-ASP119-GLY120-LYS121-ASP122-TYR123 FHR178-LEU179-GLN180-ARG181-ALA182-ASP183-PRO184

FIG. 11 15/15

FIG. 12

FIG. 12



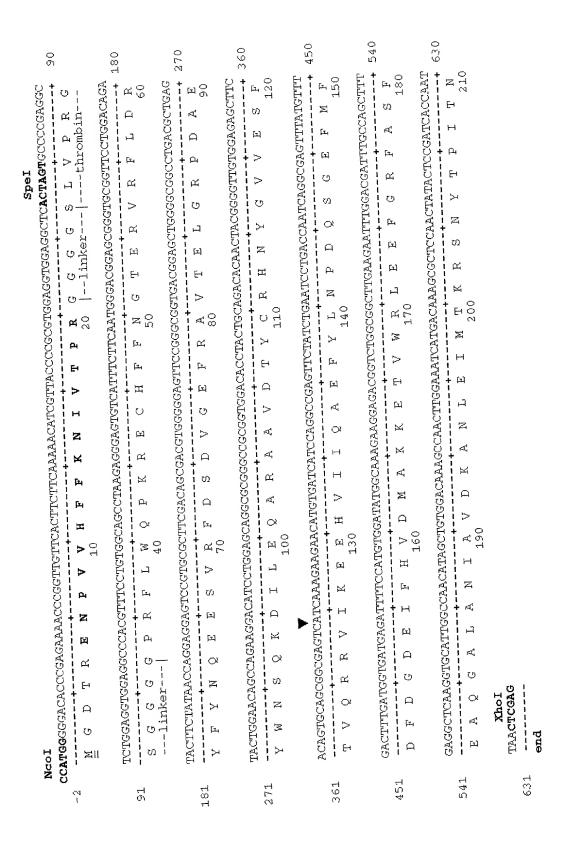
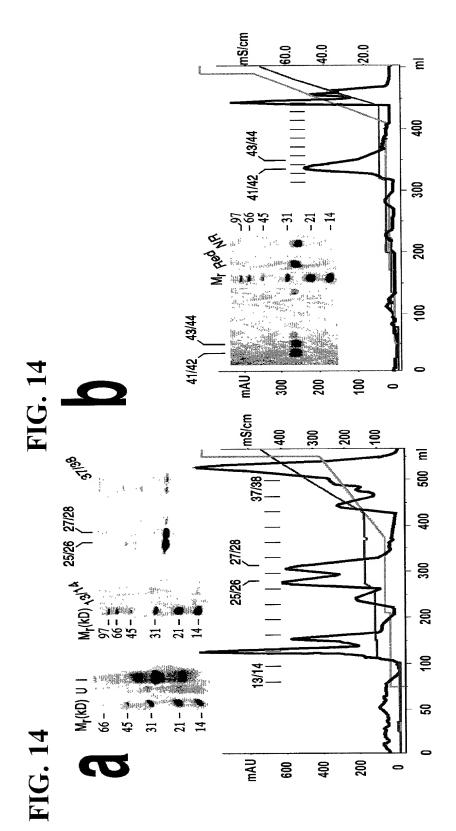


FIG. 13



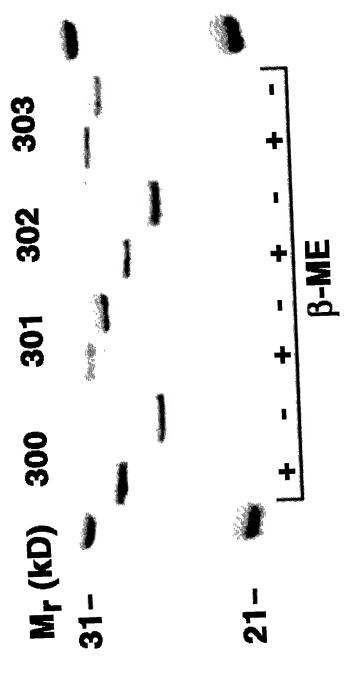


FIG. 15

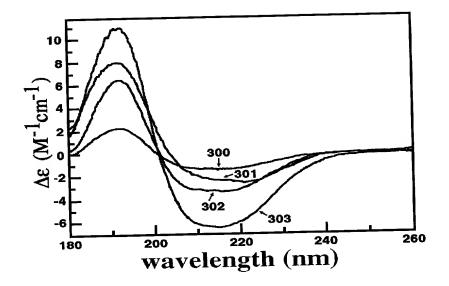


FIG. 16

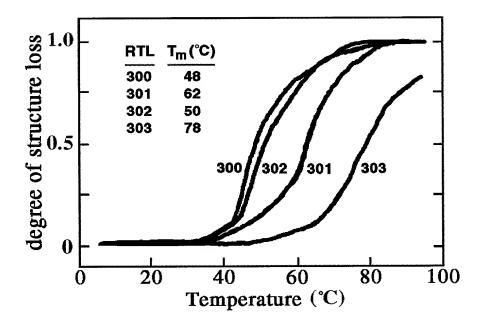


FIG. 17

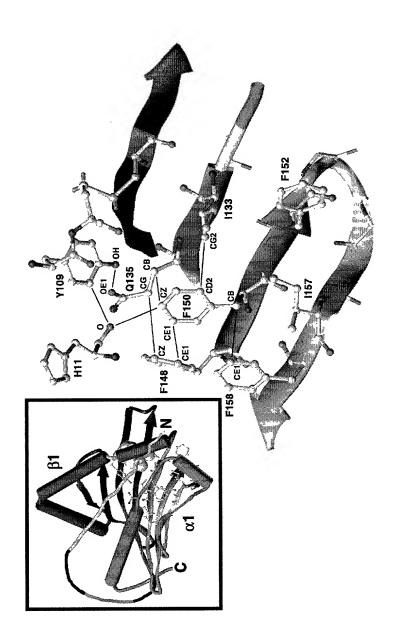


FIG. 18

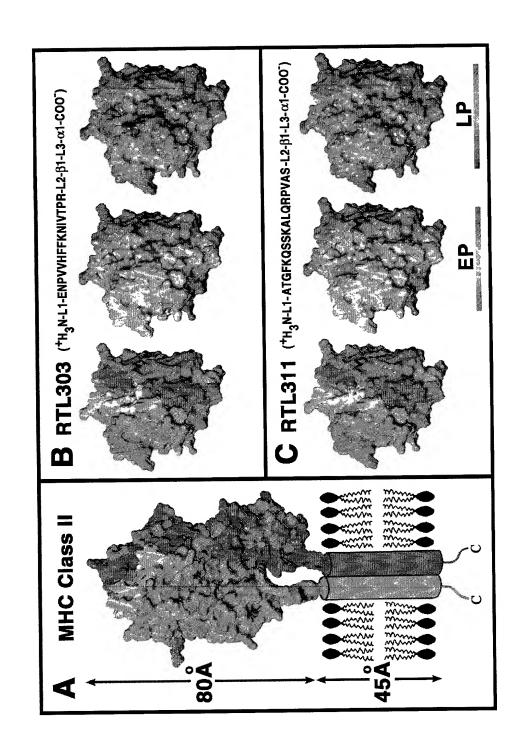
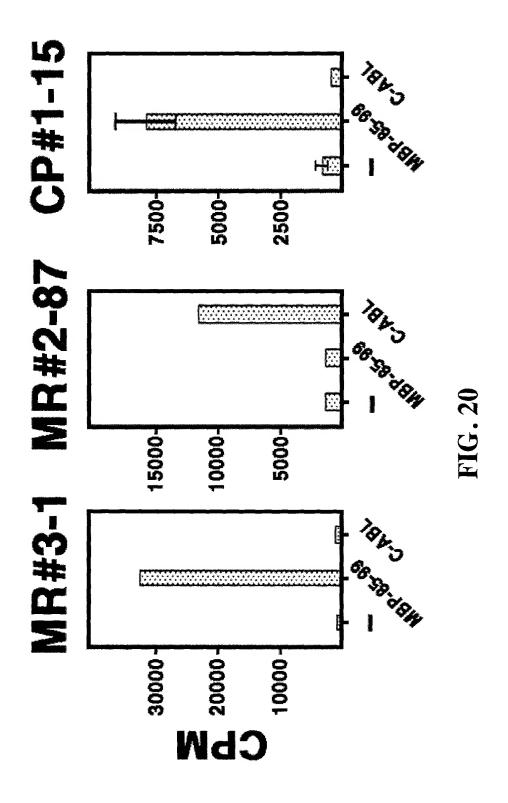
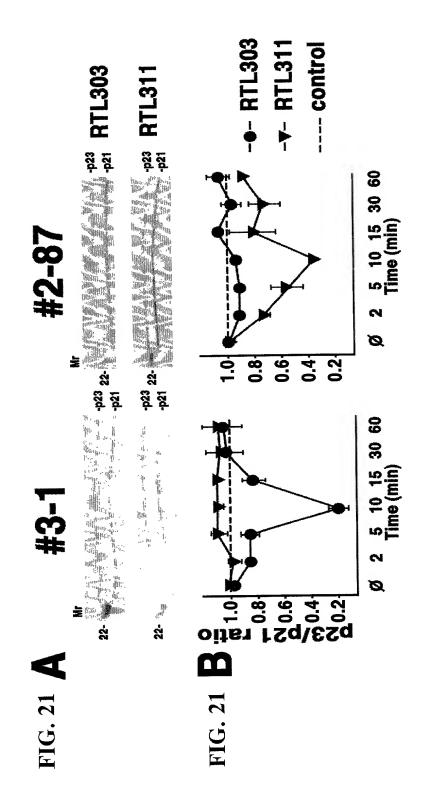


FIG. 19





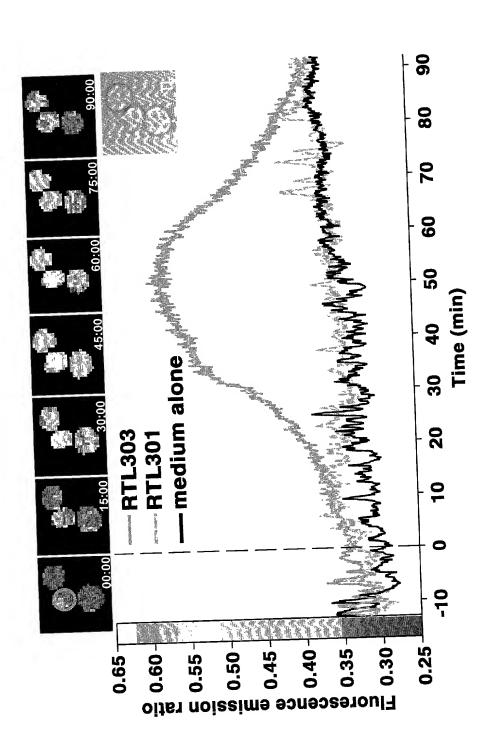


FIG. 22

